



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/424,028

Source: 165b

Date Processed by STIC: 3/21/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

RECEIVED  
MAR 29 2001  
TECH CENTER 1600/2901

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/424028

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 \_\_\_\_\_ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 \_\_\_\_\_ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 J \_\_\_\_\_ Use of <220>Feature (NEW RULES)      Sequence(s) 1,4-19 are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply  
Corrected Diskette Needed

see pgs 1-4

55 annntacagc tgcattccctt ggcgctgagg

30

see item 12 on Enr Summary Sheet

do not put this response  
on C2217 line; it  
goes on C2237 line;  
C2217 responses  
are found in  
WIPO STANDARD ST, 25,  
Appendix 2, Tables  
5 and 6

see Item 12 on Ever Summary Sheet

do not put this response  
on 12217 here

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:38

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

58 <210> SEQ ID NO: 5  
59 <211> LENGTH: 30  
60 <212> TYPE: DNA  
61 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 62 <220> FEATURE:  
W--> 63 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
64 <222> LOCATION: 1, 3-4  
65 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 66 <400> SEQUENCE: 5  
67 nanntacagc tgcattccctg ggcctgtaag 30  
68 <210> SEQ ID NO: 6  
69 <211> LENGTH: 30  
70 <212> TYPE: DNA  
71 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 72 <220> FEATURE:  
W--> 73 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
74 <222> LOCATION: 2-4  
75 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 76 <400> SEQUENCE: 6  
OK 77 cnnntacagc tgcattccctt gacgggtctc 30  
78 <210> SEQ ID NO: 7  
79 <211> LENGTH: 30  
80 <212> TYPE: DNA  
81 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 82 <220> FEATURE:  
W--> 83 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
84 <222> LOCATION: 1, 3-4  
85 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 86 <400> SEQUENCE: 7  
OK 87 ncnnntacagc tgcattccctg cccgcacagt 30  
88 <210> SEQ ID NO: 8  
89 <211> LENGTH: 30  
90 <212> TYPE: DNA  
91 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 92 <220> FEATURE:  
W--> 93 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
94 <222> LOCATION: 2-4  
95 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 96 <400> SEQUENCE: 8  
OK 97 gnnntacagc tgcattccctt cgctcggac 30  
98 <210> SEQ ID NO: 9  
99 <211> LENGTH: 30  
100 <212> TYPE: DNA  
101 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 102 <220> FEATURE:  
W--> 103 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
104 <222> LOCATION: 1, 3-4  
105 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 106 <400> SEQUENCE: 9

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
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Input Set : A:\ES.txt  
 Output Set: N:\CRF3\03212001\I424028.raw

OK 111 ngntacagc tgcattccctg atccgctagc 30  
 113 <210> SEQ ID NO: 10  
 114 <211> LENGTH: 30  
 115 <212> TYPE: DNA  
 116 <213> ORGANISM: Artificial Sequence *Item 12*  
 W--> 117 <220> FEATURE:  
 W--> 118 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 119 <222> LOCATION: 2-4  
 120 <223> OTHER INFORMATION: a, c, g, t, or u  
 OK 121 <400> SEQUENCE: 10 30  
 122 tnnntacagc tgcattccctt ccgaacccgc  
 124 <210> SEQ ID NO: 11  
 125 <211> LENGTH: 30  
 126 <212> TYPE: DNA  
 127 <213> ORGANISM: Artificial Sequence *Item 12*  
 W--> 128 <220> FEATURE:  
 W--> 129 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 130 <222> LOCATION: 1, 3-4  
 131 <223> OTHER INFORMATION: a, c, g, t, or u  
 OK 132 <400> SEQUENCE: 11 30  
 133 ntntacagc tgcattccctg agggggatag  
 135 <210> SEQ ID NO: 12  
 136 <211> LENGTH: 30  
 137 <212> TYPE: DNA  
 138 <213> ORGANISM: Artificial Sequence *Item 12*  
 W--> 139 <220> FEATURE:  
 W--> 140 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 141 <222> LOCATION: 1-2, 4  
 142 <223> OTHER INFORMATION: a, c, g, t, or u  
 OK 143 <400> SEQUENCE: 12 30  
 144 nnantacagc tgcattccctt cccgctacac  
 146 <210> SEQ ID NO: 13  
 147 <211> LENGTH: 30  
 148 <212> TYPE: DNA  
 149 <213> ORGANISM: Artificial Sequence *Item 12*  
 W--> 150 <220> FEATURE:  
 W--> 151 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 152 <222> LOCATION: 1-3  
 153 <223> OTHER INFORMATION: a, c, g, t, or u  
 OK 154 <400> SEQUENCE: 13 30  
 155 nnnatacagc tgcattccctg actccccgag  
 157 <210> SEQ ID NO: 14  
 158 <211> LENGTH: 30  
 159 <212> TYPE: DNA  
 160 <213> ORGANISM: Artificial Sequence *Item 12*  
 W--> 161 <220> FEATURE:  
 W--> 162 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 163 <222> LOCATION: 1-2, 4  
 164 <223> OTHER INFORMATION: a, c, g, t, or u

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:38

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

OK 165 <400> SEQUENCE: 14  
W--> 166 nnctacagc tgcattccctg tgttgccgagg 30  
168 <210> SEQ ID NO: 15  
169 <211> LENGTH: 30  
170 <212> TYPE: DNA  
171 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 172 <220> FEATURE:  
W--> 173 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
174 <222> LOCATION: 1-3  
175 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 176 <400> SEQUENCE: 15  
W--> 177 nnnctacagc tgcattccctc tacagcagcg 30  
179 <210> SEQ ID NO: 16  
180 <211> LENGTH: 30  
181 <212> TYPE: DNA  
182 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 183 <220> FEATURE:  
W--> 184 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
185 <222> LOCATION: 1-2, 4  
186 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 187 <400> SEQUENCE: 16  
W--> 188 nngntacagc tgcattccctg tcgcgtcggtt 30  
190 <210> SEQ ID NO: 17  
191 <211> LENGTH: 30  
192 <212> TYPE: DNA  
193 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 194 <220> FEATURE:  
W--> 195 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
196 <222> LOCATION: 1-3  
197 <223> OTHER INFORMATION: a, c, g, t, or u  
OK 198 <400> SEQUENCE: 17  
W--> 199 nnngtacagc tgcattccctc ggagcaacct 30  
201 <210> SEQ ID NO: 18  
202 <211> LENGTH: 30  
203 <212> TYPE: DNA  
204 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 205 <220> FEATURE:  
W--> 206 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
207 <222> LOCATION: 1,2,4  
208 <223> OTHER INFORMATION: a, c, g, t, or u  
W--> 209 <400> SEQUENCE: 18  
W--> 210 nntntacagc tgcattccctg gtgaccgtag 30  
212 <210> SEQ ID NO: 19  
213 <211> LENGTH: 30  
214 <212> TYPE: DNA  
215 <213> ORGANISM: Artificial Sequence *Item 12*  
W--> 216 <220> FEATURE:  
W--> 217 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
218 <222> LOCATION: 1-3

RAW SEQUENCE LISTING  
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Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

219 <223> OTHER INFORMATION: a, c, g, t, or u  
220 <400> SEQUENCE: 19  
221 nnnttacagc tgcattccctc ccctgtcgga

30

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:39

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:6 M:283 W: Missing Blank Line separator, <130> field identifier  
L:7 M:283 W: Missing Blank Line separator, <140> field identifier  
L:11 M:283 W: Missing Blank Line separator, <160> field identifier  
L:18 M:283 W: Missing Blank Line separator, <220> field identifier  
L:19 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:22 M:283 W: Missing Blank Line separator, <400> field identifier  
L:23 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:24 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:31 M:283 W: Missing Blank Line separator, <220> field identifier  
L:33 M:283 W: Missing Blank Line separator, <400> field identifier  
L:41 M:283 W: Missing Blank Line separator, <220> field identifier  
L:43 M:283 W: Missing Blank Line separator, <400> field identifier  
L:50 M:283 W: Missing Blank Line separator, <220> field identifier  
L:51 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:54 M:283 W: Missing Blank Line separator, <400> field identifier  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier  
L:63 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:66 M:283 W: Missing Blank Line separator, <400> field identifier  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:73 M:283 W: Missing Blank Line separator, <220> field identifier  
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:77 M:283 W: Missing Blank Line separator, <400> field identifier  
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:84 M:283 W: Missing Blank Line separator, <220> field identifier  
L:85 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:88 M:283 W: Missing Blank Line separator, <400> field identifier  
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:95 M:283 W: Missing Blank Line separator, <220> field identifier  
L:96 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:99 M:283 W: Missing Blank Line separator, <400> field identifier  
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:106 M:283 W: Missing Blank Line separator, <220> field identifier  
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:110 M:283 W: Missing Blank Line separator, <400> field identifier  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:117 M:283 W: Missing Blank Line separator, <220> field identifier  
L:118 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:121 M:283 W: Missing Blank Line separator, <400> field identifier  
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:128 M:283 W: Missing Blank Line separator, <220> field identifier  
L:129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:132 M:283 W: Missing Blank Line separator, <400> field identifier  
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:139 M:283 W: Missing Blank Line separator, <220> field identifier  
L:140 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:143 M:283 W: Missing Blank Line separator, <400> field identifier

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001

TIME: 14:53:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\03212001\I424028.raw

L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:150 M:283 W: Missing Blank Line separator, <220> field identifier  
L:151 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:154 M:283 W: Missing Blank Line separator, <400> field identifier  
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:161 M:283 W: Missing Blank Line separator, <220> field identifier  
L:162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:165 M:283 W: Missing Blank Line separator, <400> field identifier  
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:172 M:283 W: Missing Blank Line separator, <220> field identifier  
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:176 M:283 W: Missing Blank Line separator, <400> field identifier  
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:183 M:283 W: Missing Blank Line separator, <220> field identifier  
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:187 M:283 W: Missing Blank Line separator, <400> field identifier  
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:194 M:283 W: Missing Blank Line separator, <220> field identifier  
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
L:198 M:283 W: Missing Blank Line separator, <400> field identifier  
L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:205 M:283 W: Missing Blank Line separator, <220> field identifier  
L:206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
L:209 M:283 W: Missing Blank Line separator, <400> field identifier  
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:216 M:283 W: Missing Blank Line separator, <220> field identifier  
L:217 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
L:220 M:283 W: Missing Blank Line separator, <400> field identifier  
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19